

#28  
7-25-01

OIPE

## RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/08/971,172A

TIME: 15:27:30

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07252001\H971172A.raw

## SEQUENCE LISTING

ENTERED

2 (1) GENERAL INFORMATION:

3 (i) APPLICANT: Goodman, Corey S.

4 Kidd, Thomas

5 Mitchell, Kevin

6 Tear, Guy

7 (ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and

8 Nucleic Acids

9 (iii) NUMBER OF SEQUENCES: 13

10 (iv) CORRESPONDENCE ADDRESS:

11 (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

12 (B) STREET: 75 DENISE DRIVE

13 (C) CITY: HILLSBOROUGH

14 (D) STATE: CALIFORNIA

15 (E) COUNTRY: USA

16 (F) ZIP: 94010

17 (v) COMPUTER READABLE FORM:

18 (A) MEDIUM TYPE: Floppy disk

19 (B) COMPUTER: IBM PC compatible

20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

21 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

22 (vi) CURRENT APPLICATION DATA:

C--> 23 (A) APPLICATION NUMBER: US/08/971,172A

C--> 24 (B) FILING DATE: 14-Nov-1997

25 (C) CLASSIFICATION:

26 (viii) ATTORNEY/AGENT INFORMATION:

27 (A) NAME: OSMAN, RICHARD A

28 (B) REGISTRATION NUMBER: 36,627

29 (C) REFERENCE/DOCKET NUMBER: B98-006

30 (ix) TELECOMMUNICATION INFORMATION:

31 (A) TELEPHONE: (650) 343-4341

32 (B) TELEFAX: (650) 343-4342

34 (2) INFORMATION FOR SEQ ID NO: 1:

35 (i) SEQUENCE CHARACTERISTICS:

36 (A) LENGTH: 4188 base pairs

37 (B) TYPE: nucleic acid

38 (C) STRANDEDNESS: double

39 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

41 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

42 ATGCATCCCA TGCATCCCGA AAACCACGCC ATCGCCCGGA GCACGAGCAC CACTAATAAC	60
43 CCATCTCGCA GTCGGAGCAG CAGGATGTGG CTCCTGCCCG CCTGGCTGCT CCTCGTCTTG	120
44 GTGGCCAGCA ATGGCCTGCC AGCAGTCAGA GGCCAGTACC AATCGCCACG TATCATCGAG	180
45 CATCCACGG ATCTGGTCGT TAAGAAGAAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG	240
46 GGCAAGCCGG AACCCACCAT TGAGTGGTTT AAGGATGGCG AACCCGTCAG CACCAACGAA	300
47 AAGAAATCGC ACCGCGTCCA GTTCAAGGAC GGCGCCCTCT TCTTTTACAG GACAATGCAA	360
48 GGCAAGAAGG AGCAGGACGG CGGAGAGTAC TGGTGCGTGG CCAAGAACCG AGTGGGCCAG	420

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49	GCCGTTAGTC	GCCATGCCTC	CCTCCAGATA	GCTGTTTTGC	GCGACGATTT	TCGCGTGGAG	480
50	CCCAAAGACA	CGCGAGTGGC	CAAAGGCGAG	ACGGCTCTGC	TGGAGTGTGG	GCCGCCCAAA	540
51	GGCATTCCAG	AGCCAACGCT	GATTTGGATA	AAGGACGGCG	TTCCCTTGGA	CGACCTGAAA	600
52	GCCATGTCGT	TTGGCGCCAG	CTCCCGCGTT	CGAATTGTGG	ACGGTGGCAA	CCTGCTGATC	660
53	AGCAATGTGG	AGCCCATTGA	TGAGGGCAAC	TACAAGTGCA	TTGCCAGAA	TCTGGTAGGC	720
54	ACCCGCGAGA	GCAGCTATGC	CAAGCTGATT	GTCCAGGTCA	AACCATACTT	TATGAAGGAG	780
55	CCCAAGGATC	AGGTGATGCT	CTACGGCCAG	ACAGCCACTT	TCCACTGCTC	AGTGGGCGGT	840
56	GATCCGCCGC	CGAAAGTGTT	GTGGAAAAAG	GAGGAGGGCA	ATATTCCGGT	GTCCAGAGCG	900
57	CGAATCCTTC	ACGACGAGAA	AAGTTTAGAG	ATATCCAACA	TAACGCCAC	CGATGAGGGC	960
58	ACCTATGTCT	GCGAGGCACA	CAACAATGTC	GGTCAGATCA	GCGCTAGGGC	TTCTCTTATA	1020
59	GTCCACGCTC	CGCCGAACCT	TACGAAAAGA	CCCAGTAACA	AGAAAGTGGG	ACTAAATGGG	1080
60	GTTGTCCAAC	TACCTTGCAT	GGCCTCCGGA	AACCCTCCGC	CGTCTGTATT	CTGGACCAAG	1140
61	GAAGGAGTAT	CCACTCTTAT	GTTCCCAAAT	AGTTCGCACG	GAAGGCAGTA	TGTGGCTGCC	1200
62	GATGGAATC	TGCAGATTAC	GGATGTGCGG	CAGGAAGACG	AAGGCTACTA	TGTGTGTTCC	1260
63	GCTTTCAGTG	TAGTCGATTC	CTCTACAGTA	CGGGTTTTCC	TGCAAGTCAG	CTCGGTAGAC	1320
64	GAGCGTCCAC	CTCCGATTAT	TCAAATCGGA	CTTGCCAATC	AAACACTGCC	CAAGGGATCA	1380
65	GTTGCTACTT	TACCCTGTGC	GGCCACTGGA	AATCCCAGTC	CCCGTATCAA	GTGGTTCCAC	1440
66	GATGGACATG	CCGTACAAGC	GGGCAATCGA	TACAGCATCA	TCCAAGGAAG	CTCACTGAGA	1500
67	GTCGATGACC	TTCAACTAAG	TGACTCTGGT	ACCTACACCT	GCACTGCATC	TGGCGAACGA	1560
68	GGAGAACTT	CCTGGGCTGC	CACACTAACG	GTGGAAAAAC	CCGGTTCTAC	ATCTCTTCAC	1620
69	CGGGCAGCTG	ATCCTAGCAC	TTATCCTGCT	CCTCCAGGAA	CACCTAAAGT	CCTGAATGTC	1680
70	AGTCGCACCA	GCATTAGTCT	TCGTTGGGCT	AAAAGCCAAG	AGAAACCCGG	AGCTGTGGGC	1740
71	CCAATCATTG	GATACACTGT	AGAGTACTTC	AGTCCGGATC	TGCAAACTGG	TTGGATTGTG	1800
72	GCTGCCCATC	GAGTCGGCGA	CACTCAAGTC	ACTATCTCGG	GTCTCACTCC	TGGCACTTCG	1860
73	TATGTGTTCC	TAGTTAGAGC	TGAGAATACT	CAGGGTATTT	CTGTGCCTTC	CGGCTTATCA	1920
74	AATGTTATTA	AAACCATTTGA	GGCAGATTTT	GATGCAGCTT	CTGCCAATGA	TTTGTGAGCA	1980
75	GCTCGAACTT	TGCTGACAGG	AAAGTCGGTG	GAGCTAATAG	ATGCCTCGGC	TATCAATGCT	2040
76	AGTGCCGTTA	GACTTGAGTG	GATGCTCCAC	GTGAGCGCTG	ATGAGAAATA	CGTAGAGGGC	2100
77	CTGCGCATAC	ACTATAAGGA	TGCCAGTGTA	CCATCCGCAC	AGTATCACTC	GATCACTGTT	2160
78	ATGGATGCCT	CTGCAGAATC	GTTTGTGGTG	GGAAACCTTA	AGAAGTACAC	CAAGTATGAG	2220
79	TTCTTCTTAA	CACCTTTTTT	TGAGACAATT	GAAGGACAGC	CCAGTAACTC	CAAGACAGCC	2280
80	CTCACCTATG	AAGATGTTCC	CTCCGCACCA	CCGGATAACA	TTCAGATTGG	CATGTACAAC	2340
81	CAAACAGCCG	GTTGGGTGCG	TTGGACTCCG	CCACCTCCC	AGCACCACAA	TGGCAATTTG	2400
82	TATGGCTACA	AGATTGAGGT	CAGCGCCGGT	AACACCATGA	AGGTGCTGGC	CAATATGACT	2460
83	CTTAATGCTA	CCACCACATC	TGTGCTCCTA	AATAACCTAA	CCACCGGAGC	TGTGTACAGC	2520
84	GTGAGGTTGA	ACTCCTTTAC	CAAGGCAGGA	GATGGACCTT	ACTCCAAACC	GATATCACTA	2580
85	TTCATGGACC	CCACCCATCA	TGTGCATCCG	CCACGGGCAC	ATCCAAGCGG	CACCCATGAT	2640
86	GGGCGACATC	AGGGACAGGA	TCTCACGTAT	CATAACAATG	GCAACATACC	ACCTGGCGAC	2700
87	ATTAATCCCA	CCACTCATAA	AAAGACCAC	GACTACCTAT	CTGGACCGTG	GCTAATGGTG	2760
88	CTGGTCTGCA	TCGTTCTTCT	AGTCCTGGTT	ATTTCCGGCG	CTATTTTCGAT	GGTCTACTTC	2820
89	AAGCGCAAGC	ATCAAATGAC	CAAGGAATTG	GGTCACTTAA	GTGTGGTCAG	TGACAACGAA	2880
90	ATAACCGCAT	TAAATATCAA	TAGCAAAGAG	AGCCTTTGGA	TAGACCATCA	TCGTGGATGG	2940
91	CGAAGTCCG	ATACTGACAA	AGACTCAGGA	TTAAGCGAAT	CGAAGCTACT	ATCCCACGTT	3000
92	AACAGCAGTC	AATCCAAC	CAATAACTCC	GATGGAGGAA	CCGATTATGC	AGAAGTTGAC	3060
93	ACCCGTAACC	TTACCACCTT	CTACAATTGT	CGCAAGAGCC	CCGATAATCC	CACGCCGTAC	3120
94	GCCACCACTA	TGATCATTGG	TACCTCTTCC	AGTGAGACCT	GCACCAAGAC	AACATCTATA	3180
95	AGTGCCGATA	AGGACTCGGG	AACCTCATTC	CCCTATTCTG	ACGCATTTGC	CGGTCAGGTG	3240
96	CCAGCGGTTT	CTGTTGTCAA	ATCCAAC	CTTCAGTATC	CGGTTGAACC	GATCAACTGG	3300
97	TCAGAGTTTC	TACCCCGGCC	GCCAGAACAC	CCACCTCCGT	CTTCTACCTA	TGGATACGCA	3360

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98 CAAGGATCTC CTGAATCTTC GCGGAAGAGC TCCAAAAGCG CAGGTTCCGG CATTTCTACA 3420
99 AATCAAAGCA TTCTGAACGC ATCCATACAC AGCAGCTCCT CGGGCGGCTT TTCAGCTTGG 3480
100 GGAGTATCGC CCAATATATGC TGTCGCCTGT CCACCGGAAA ACGTTTATAG CAATCCGCTG 3540
101 TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCACAAA CCAACATCCG 3600
102 CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC 3660
103 CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG 3720
104 CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCATGCCT TGGCCACACC CTCGCCCATG 3780
105 CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCAGGTGCA TCCCAATAGC 3840
106 CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG 3900
107 GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC 3960
108 AGTGCCAAAC AACCGGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG 4020
109 GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC 4080
110 TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC 4140
111 GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA 4188

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113 (2) INFORMATION FOR SEQ ID NO: 2:

114 (i) SEQUENCE CHARACTERISTICS:

115 (A) LENGTH: 1395 amino acids

116 (B) TYPE: amino acid

117 (C) STRANDEDNESS: single

118 (D) TOPOLOGY: linear

119 (ii) MOLECULE TYPE: peptide

120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

121 Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
122 1 5 10 15
123 Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Ser Arg Met Trp Leu Leu
124 20 25 30
125 Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
126 35 40 45
127 Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
128 50 55 60
129 Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
130 65 70 75 80
131 Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
132 85 90 95
133 Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
134 100 105 110
135 Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
136 115 120 125
137 Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
138 130 135 140
139 His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
140 145 150 155 160
141 Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
142 165 170 175
143 Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
144 180 185 190
145 Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
146 195 200 205
147 Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu

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148	210	215	220													
149	Pro	Ile	Asp	Glu	Gly	Asn	Tyr	Lys	Cys	Ile	Ala	Gln	Asn	Leu	Val	Gly
150	225					230					235					240
151	Thr	Arg	Glu	Ser	Ser	Tyr	Ala	Lys	Leu	Ile	Val	Gln	Val	Lys	Pro	Tyr
152					245					250						255
153	Phe	Met	Lys	Glu	Pro	Lys	Asp	Gln	Val	Met	Leu	Tyr	Gly	Gln	Thr	Ala
154				260					265					270		
155	Thr	Phe	His	Cys	Ser	Val	Gly	Gly	Asp	Pro	Pro	Pro	Lys	Val	Leu	Trp
156			275					280					285			
157	Lys	Lys	Glu	Glu	Gly	Asn	Ile	Pro	Val	Ser	Arg	Ala	Arg	Ile	Leu	His
158			290			295						300				
159	Asp	Glu	Lys	Ser	Leu	Glu	Ile	Ser	Asn	Ile	Thr	Pro	Thr	Asp	Glu	Gly
160	305					310					315					320
161	Thr	Tyr	Val	Cys	Glu	Ala	His	Asn	Asn	Val	Gly	Gln	Ile	Ser	Ala	Arg
162				325						330						335
163	Ala	Ser	Leu	Ile	Val	His	Ala	Pro	Pro	Asn	Phe	Thr	Lys	Arg	Pro	Ser
164				340					345					350		
165	Asn	Lys	Lys	Val	Gly	Leu	Asn	Gly	Val	Val	Gln	Leu	Pro	Cys	Met	Ala
166			355					360					365			
167	Ser	Gly	Asn	Pro	Pro	Pro	Ser	Val	Phe	Trp	Thr	Lys	Glu	Gly	Val	Ser
168			370			375						380				
169	Thr	Leu	Met	Phe	Pro	Asn	Ser	Ser	His	Gly	Arg	Gln	Tyr	Val	Ala	Ala
170	385					390					395					400
171	Asp	Gly	Thr	Leu	Gln	Ile	Thr	Asp	Val	Arg	Gln	Glu	Asp	Glu	Gly	Tyr
172				405						410						415
173	Tyr	Val	Cys	Ser	Ala	Phe	Ser	Val	Val	Asp	Ser	Ser	Thr	Val	Arg	Val
174				420					425					430		
175	Phe	Leu	Gln	Val	Ser	Ser	Val	Asp	Glu	Arg	Pro	Pro	Pro	Ile	Ile	Gln
176			435					440					445			
177	Ile	Gly	Pro	Ala	Asn	Gln	Thr	Leu	Pro	Lys	Gly	Ser	Val	Ala	Thr	Leu
178		450				455					460					
179	Pro	Cys	Arg	Ala	Thr	Gly	Asn	Pro	Ser	Pro	Arg	Ile	Lys	Trp	Phe	His
180	465				470						475					480
181	Asp	Gly	His	Ala	Val	Gln	Ala	Gly	Asn	Arg	Tyr	Ser	Ile	Ile	Gln	Gly
182				485						490						495
183	Ser	Ser	Leu	Arg	Val	Asp	Asp	Leu	Gln	Leu	Ser	Asp	Ser	Gly	Thr	Tyr
184			500					505						510		
185	Thr	Cys	Thr	Ala	Ser	Gly	Glu	Arg	Gly	Glu	Thr	Ser	Trp	Ala	Ala	Thr
186			515					520					525			
187	Leu	Thr	Val	Glu	Lys	Pro	Gly	Ser	Thr	Ser	Leu	His	Arg	Ala	Ala	Asp
188		530				535						540				
189	Pro	Ser	Thr	Tyr	Pro	Ala	Pro	Pro	Gly	Thr	Pro	Lys	Val	Leu	Asn	Val
190	545					550					555					560
191	Ser	Arg	Thr	Ser	Ile	Ser	Leu	Arg	Trp	Ala	Lys	Ser	Gln	Glu	Lys	Pro
192				565						570						575
193	Gly	Ala	Val	Gly	Pro	Ile	Ile	Gly	Tyr	Thr	Val	Glu	Tyr	Phe	Ser	Pro
194				580					585					590		
195	Asp	Leu	Gln	Thr	Gly	Trp	Ile	Val	Ala	Ala	His	Arg	Val	Gly	Asp	Thr
196			595					600						605		

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197  Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
198      610      615      620
199  Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
200      625      630      635      640
201  Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
202      645      650      655
203  Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
204      660      665      670
205  Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
206      675      680      685
207  Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
208      690      695      700
209  Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
210      705      710      715      720
211  Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
212      725      730      735
213  Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
214      740      745      750
215  Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
216      755      760      765
217  Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
218      770      775      780
219  Trp Val Arg Trp Thr Pro Pro Pro Ser Gln His His Asn Gly Asn Leu
220      785      790      795      800
221  Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
222      805      810      815
223  Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
224      820      825      830
225  Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
226      835      840      845
227  Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
228      850      855      860
229  Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
230      865      870      875      880
231  Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
232      885      890      895
233  Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
234      900      905      910
235  Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val
236      915      920      925
237  Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
238      930      935      940
239  Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu
240      945      950      955      960
241  Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His
242      965      970      975
243  His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser
244      980      985      990
245  Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn

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## VERIFICATION SUMMARY

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L:23 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:24 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:1196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

L:1210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10